The Graphical Sequence Viewer

Graphical presentation of sequence data

https://www.ncbi.nlm.nih.gov/projects/sviewer/

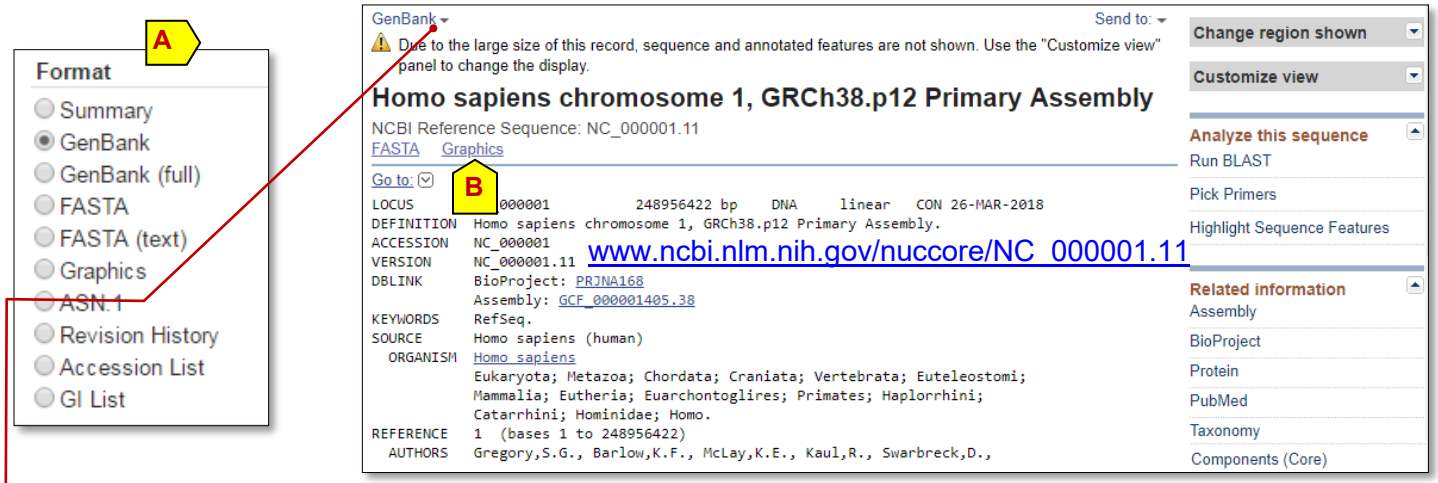
National Center for Biotechnology Information • National Library of Medicine • National Institutes of Health • Department of Health and Human Services

Scope and Access

The Sequence Viewer (SV) from NCBI is a free, web-based tool for graphical display and analysis of genomic, mRNA, and protein sequences. It is a flexible interface that combines a bird's eye view of a complete chromosome with a detailed interrogation at a single nucleotide resolution. You can access this display from individual records in Nucleotide, Protein, Gene, Genome, SNP, dbGaP, dbVar and Clone databases, and from various tools such as BLAST and Primer BLAST. You can also import and render custom data in different formats into SV. For more details see the SV help document linked on the project's homepage at https://www.ncbi.nlm.nih.gov/projects/sviewer/

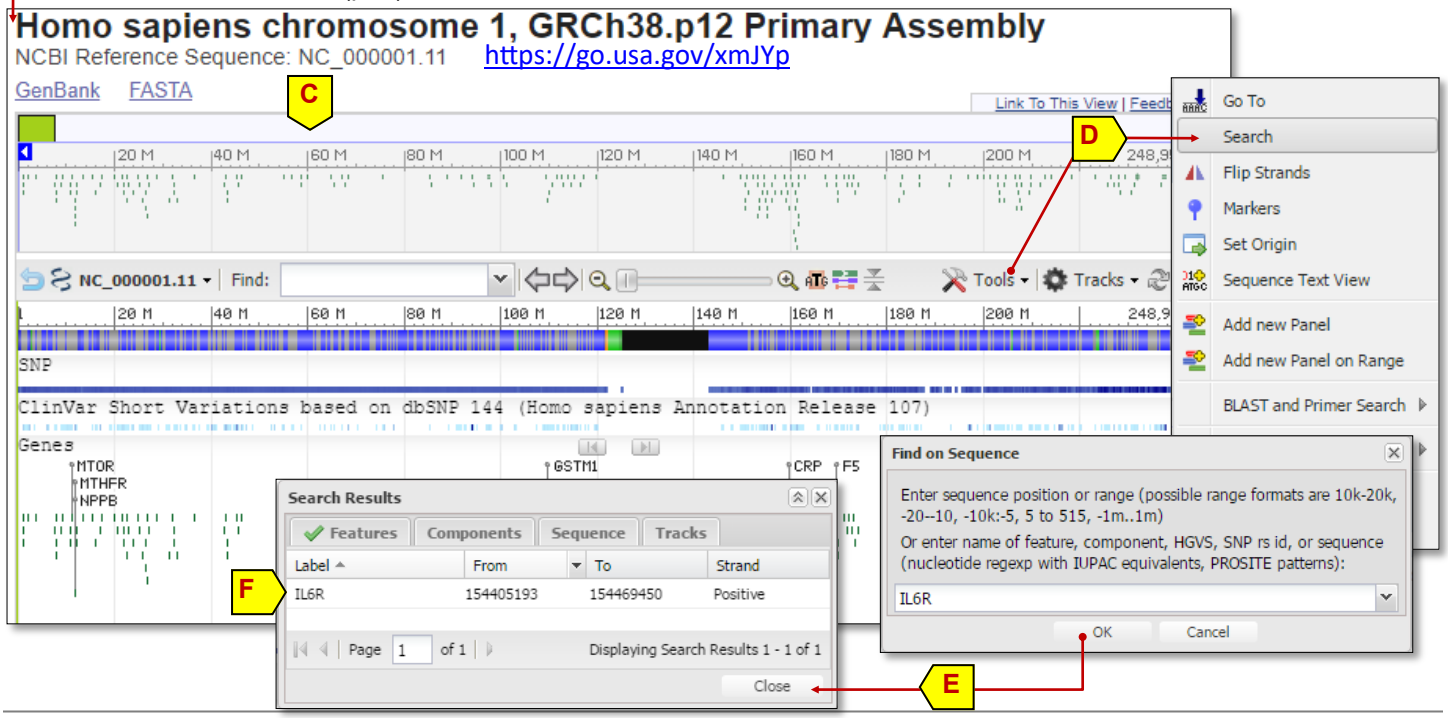
Activating an SV Display Through the *Graphics* Link

A common use of SV is to display a large genome. For example, you can retrieve the human chromosome 1 record from the Nucleotide database by its accession number NC_000001, and display it graphically in SV by selecting Graphics under the display format menu under GenBank (**A**) or simply by clicking the Graphics link (**B**) at the top of the record.



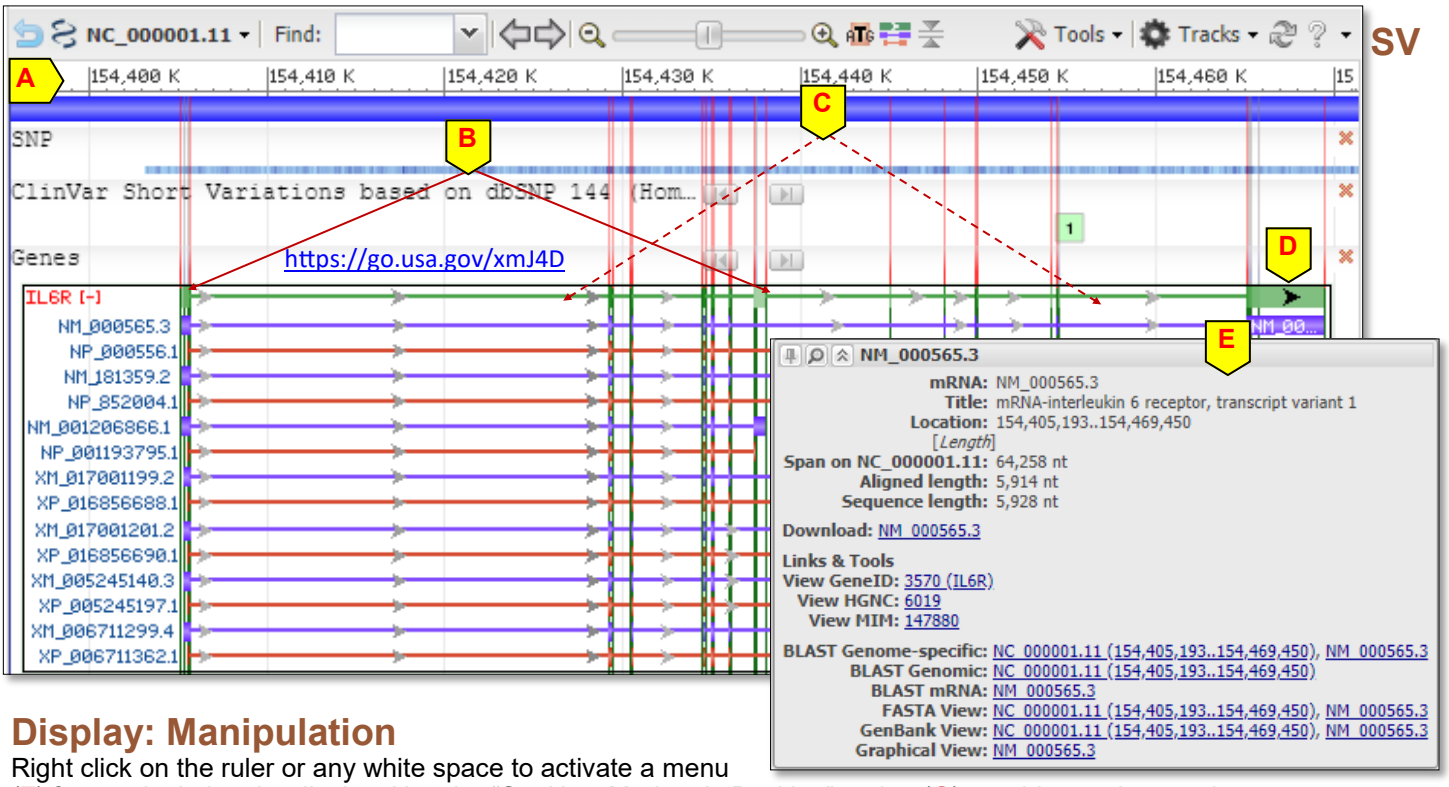
SV Display: the Overview Panel

The top-most panel of the Graphics page represents chromosome 1 in its entirety (**C**) with its ruler showing the genomic coordinates. You can search for Genes and other annotated features using the "Search" option in the "Tools" dropdown menu (**D**), where the example searches for the IL6R (**E**) gene. Click the "IL6R" gene (**F**) to zoom in to that feature for more detailed examination (p. 2).



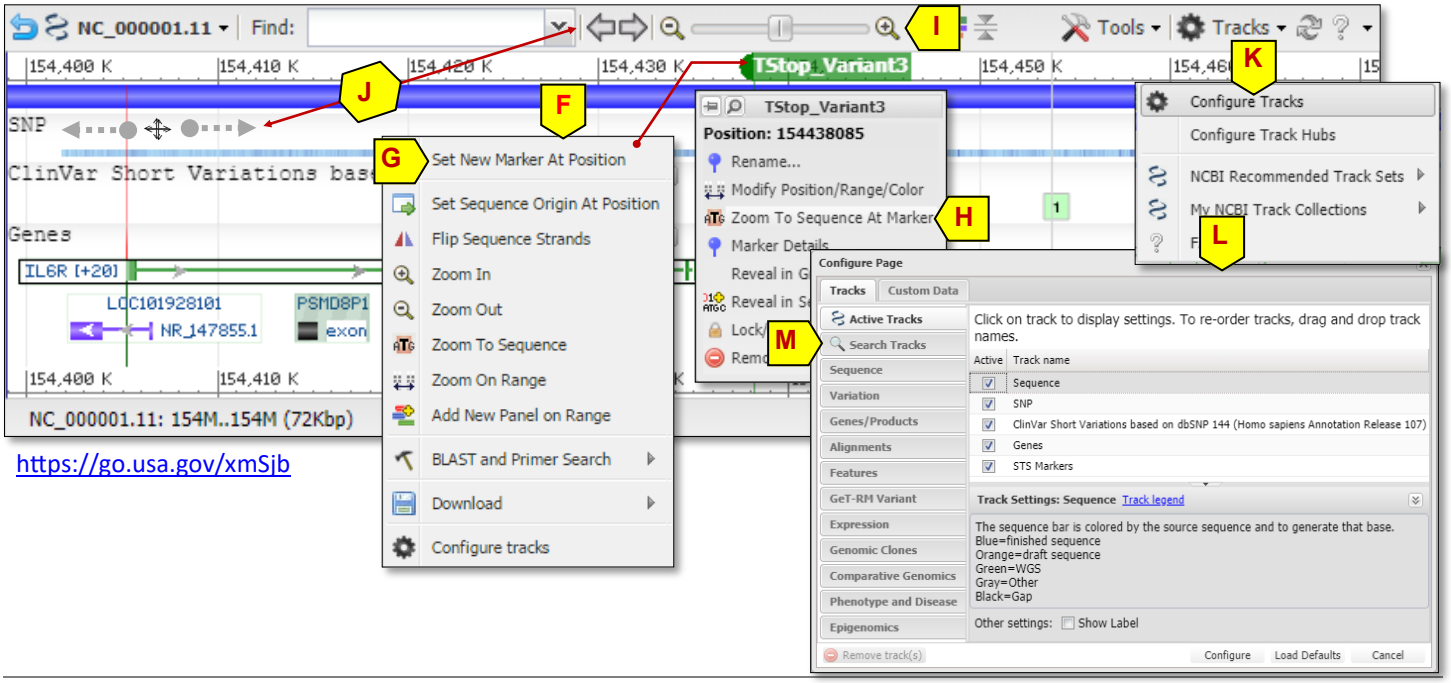
SV Display: the Graphical Panel

The graphical panel below the overview shows the details of the IL6R gene, with its genomic range shown in the ruler at the top of the panel (**A**). Click the green Gene bar to see details in the expanded section, which depicts exons as vertical lines/boxes (**B**) linked by introns (as thin lines, **C**). Arrows (**D**) in the display indicates the gene orientation. Hover over a displayed item, such as a specific transcript variant (**E**), to see additional details in a popup.



Display: Manipulation

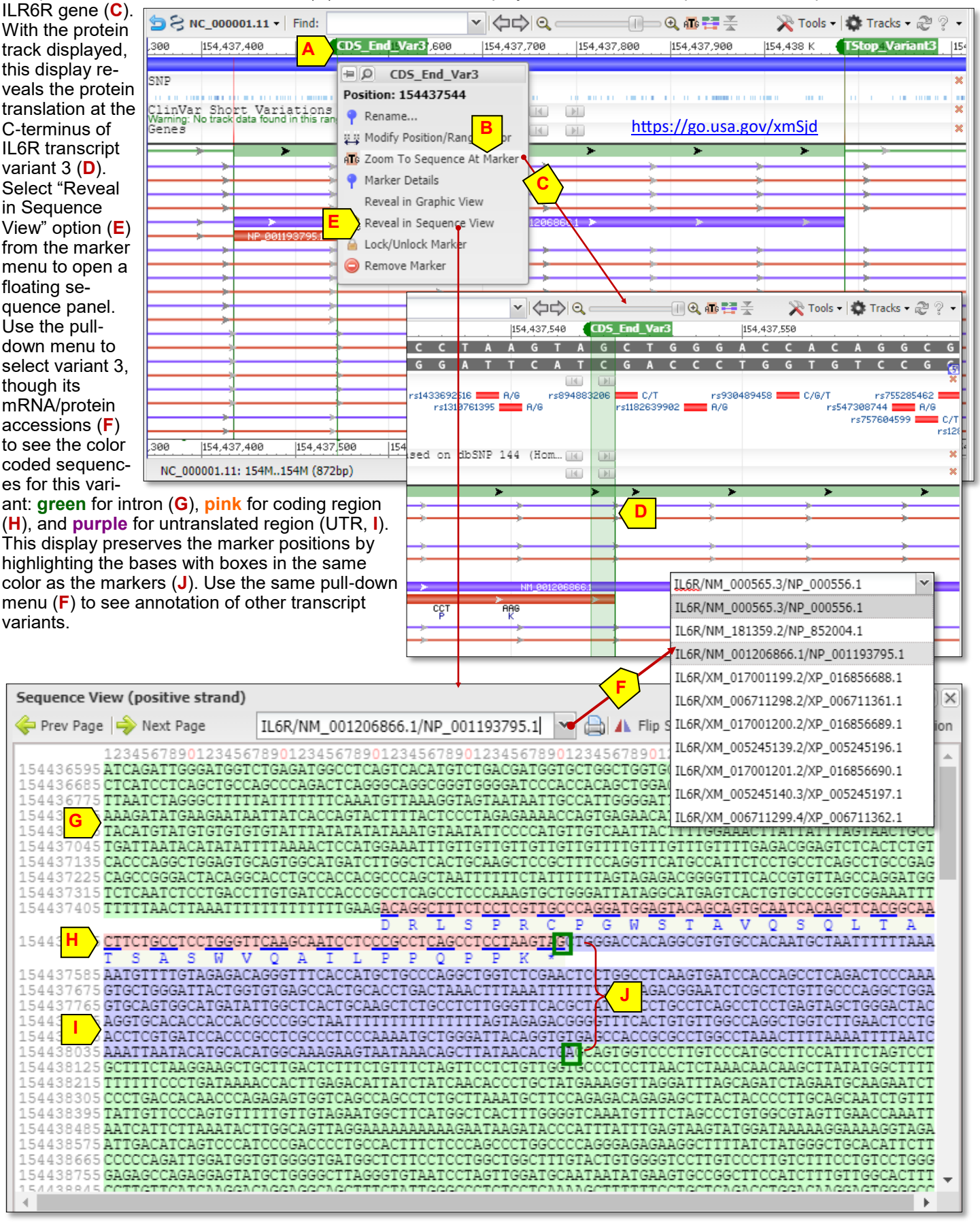
Right click on the ruler or any white space to activate a menu (**F**) for manipulating the display. Use the "Set New Marker At Position" option (**G**) to add a marker, such as "TStop_Variant3," at a desired location. The marker context menu enables single-click "Zoom To Sequence At Marker" function (**H**). Use the zoom slider (**I**) to zoom in and out incrementally. Pan the display to surrounding regions by holding the left mouse button and dragging the image horizontally, or by using the arrows at the top (**J**). Click the "Tracks" button (**K**) and select "Configure Tracks" to access available tracks in the "Configure Page" dialog box (**L**), through categories listed under the "Tracks" tab, or locate specific ones using the "Search tracks" function (**M**). Embedded SV displays from records in other NCBI database, such as records from the Gene database, provides NCBI recommended track sets in a cascading menu under Tracks (**K**). You can also save your track setting to My NCBI for reference and easy access.



https://go.usa.gov/xmSjb

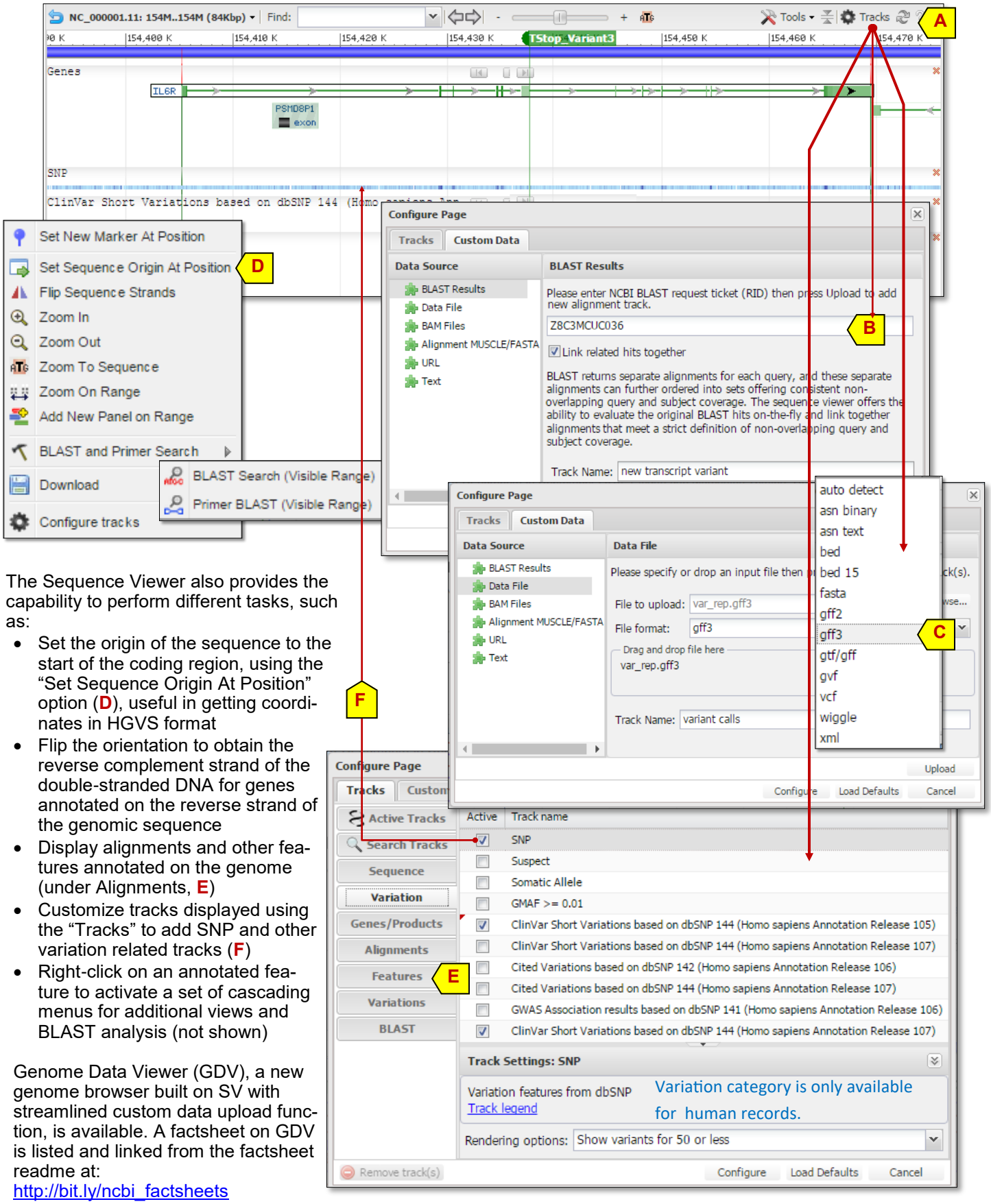
Examining a Specific Region at Single Nucleotide Resolution

A marker place at a position of interest (**A**) enables ready access to sequences through the "Zoom to Sequence At Marker" option in the marker context menu (**B**). The zoomed in display shows the CDS stop for the transcript variant 3 of the ILR6R gene (**C**). With the protein track displayed, this display reveals the protein translation at the C-terminus of IL6R transcript variant 3 (**D**). Select "Reveal in Sequence View" option (**E**) from the marker menu to open a floating sequence panel. Use the pull-down menu to select variant 3, though its mRNA/protein accessions (**F**) to see the color coded sequences for this variant: **green** for intron (**G**), **pink** for coding region (**H**), and **purple** for untranslated region (UTR, **I**). This display preserves the marker positions by highlighting the bases with boxes in the same color as the markers (**J**). Use the same pull-down menu (**F**) to see annotation of other transcript variants.



Additional Displays and Functions

Using the "Tracks" dialog box (**A**), you can also upload custom data from external sources into a Sequence Viewer display, such as a BLAST result using the assigned Request ID (**B**) or data file from other sources in various formats (**C**).



The Sequence Viewer also provides the capability to perform different tasks, such as:

- Set the origin of the sequence to the start of the coding region, using the "Set Sequence Origin At Position" option (**D**), useful in getting coordinates in HGVS format
- Flip the orientation to obtain the reverse complement strand of the double-stranded DNA for genes annotated on the reverse strand of the genomic sequence
- Display alignments and other features annotated on the genome (under Alignments, **E**)
- Customize tracks displayed using the "Tracks" to add SNP and other variation related tracks (**F**)
- Right-click on an annotated feature to activate a set of cascading menus for additional views and BLAST analysis (not shown)

Genome Data Viewer (GDV), a new genome browser built on SV with streamlined custom data upload function, is available. A factsheet on GDV is listed and linked from the factsheet readme at: http://bit.ly/ncbi_factsheets